



PCT09

RAW SEQUENCE LISTING

DATE: 05/08/2002.

PATENT APPLICATION: US/09/807,512

TIME: 13:30:28

Input Set : A:\seqlist_0652.2200000-text.txt

Output Set: N:\CRF3\05082002\I807512.raw

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5 <110> APPLICANT: Schrier, Peter I.
6   Aarnoudse, Corlien
7   Heider, Karl-Heinz
8   Klade, Christoph
10 <120> TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
11   Antigen-Lage 1
13 <130> FILE REFERENCE: 0652.2200000
15 <140> CURRENT APPLICATION NUMBER: 09/807,512
16 <141> CURRENT FILING DATE: 2001-04-16
18 <150> PRIOR APPLICATION NUMBER: PCT/EP99/07832
19 <151> PRIOR FILING DATE: 1999-10-15
21 <150> PRIOR APPLICATION NUMBER: EP 98119583.7
22 <151> PRIOR FILING DATE: 1998-10-16
24 <160> NUMBER OF SEQ ID NOS: 28
26 <170> SOFTWARE: PatentIn Ver. 2.1
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 679
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
35 <221> NAME/KEY: 3'UTR
36 <222> LOCATION: (340)..(679)
38 <220> FEATURE:
39 <221> NAME/KEY: 5'UTR
40 <222> LOCATION: (1)..(9)
42 <220> FEATURE:
43 <221> NAME/KEY: CDS
44 <222> LOCATION: (10)..(339)
47 <400> SEQUENCE: 1
C--> 49   cgacgggagc atg ctg atg gcc cag gag gcc ctg gca ttc ctg atg gcc      48
50           Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala
51           1               5               10
53   cag ggg gca atg ctg gcg gcc cag gag agg cgg gtg cca cgg gcg gca      96
54   Gln Gly Ala Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala
55           15               20               25
57   gag gtc ccc ggg gcg cag ggg cag caa ggg cct cgg ggc cga gag gag      144
58   Glu Val Pro Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu
59           30               35               40               45
61   gcg ccc cgc ggg gtc cgc atg gcg gtg ccg ctt ctg cgc agg atg gaa      192
62   Ala Pro Arg Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu
63           50               55               60
67   ggt gcc cct gcg ggg cca gga ggc cgg aca gcc gcc tgc ttc agt tgc      240
68   Gly Ala Pro Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys

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69          65          70          75
71  aca tca cga tgc ctt tct cgt cgc cca tgg aag cgg agc tgg tcc gca      288
72  Thr Ser Arg Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala
73          80          85          90
75  gga tcc tgt ccc ggg atg ccg cac ctc tcc ccc gac cag ggg cgg ttc      336
76  Gly Ser Cys Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe
77          95          100          105
79  tga aggacttcac cgtgtccggc aacctactgt ttatccgact gactgctgca      389
82  gaccaccgcc aactgcagct ctccatcagc tctgtctcc agcagctttc cctgttgatg      449
84  tggatcacgc agtgccttct gcccggtgtt ttggctcagg ctccctcagg gcagaggcgc      509
86  taagcccagc ctggcgcccc ttctagggtc atgcctcctc cctaggggaa tgggtcccagc      569
88  acgagtggcc agttcattgt gggggcctga ttgtttgtcg ctggaggagg acggcttaca      629
90  tgtttgtttc tgtagaaaat aaagctgagc tacgaaaaaa aaaaaaaaaa      679

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94 <210> SEQ ID NO: 2

95 <211> LENGTH: 109

96 <212> TYPE: PRT

97 <213> ORGANISM: Homo sapiens

99 <400> SEQUENCE: 2

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101  Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala
102      1          5          10          15
104  Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro
105      20          25          30
107  Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg
108      35          40          45
110  Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu Gly Ala Pro
111      50          55          60
113  Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys Thr Ser Arg
114      65          70          75          80
116  Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala Gly Ser Cys
117      85          90          95
119  Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe
120      100          105

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124 <210> SEQ ID NO: 3

125 <211> LENGTH: 767

126 <212> TYPE: DNA

127 <213> ORGANISM: Homo sapiens

129 <220> FEATURE:

130 <221> NAME/KEY: CDS

131 <222> LOCATION: (54)..(596)

133 <220> FEATURE:

134 <221> NAME/KEY: 3'UTR

135 <222> LOCATION: (597)..(767)

137 <220> FEATURE:

138 <221> NAME/KEY: 5'UTR

139 <222> LOCATION: (1)..(53)

141 <400> SEQUENCE: 3

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C--> 143  atcctcgtgg gccctgacct tctctctgag agccgggcag aggctccgga gcc atg      56
      144                                     Met
      145                                     1

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147   cag gcc gaa ggc cag ggc aca ggg ggt tcg acg ggc gat gct gat ggc      104
148   Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly
149           5              10              15
151   cca gga ggc cct ggc att cct gat ggc cca ggg ggc aat gct ggc ggc      152
152   Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly
153           20              25              30
155   cca gga gag gcg ggt gcc acg ggc ggc aga ggt ccc cgg ggc gca ggc      200
156   Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly
157           35              40              45
159   gca gca agg gcc tcg ggg ccg aga gga ggc gcc ccg cgg ggt ccg cat      248
160   Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His
161           50              55              60              65
163   ggc ggt gcc gct tct gcg cag gat gga agg tgc ccc tgc ggg gcc agg      296
164   Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg
165           70              75              80
167   agg ccg gac agc cgc ctg ctt cag ttg cac atc acg atg cct ttc tcg      344
168   Arg Pro Asp Ser Arg Leu Leu Gln His Ile Thr Met Pro Phe Ser
169           85              90              95
171   tcg ccc atg gaa gcg gag ctg gtc cgc agg atc ctg tcc cgg gat gcc      392
172   Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala
173           100             105             110
175   gca cct ctc ccc cga cca ggg gcg gtt ctg aag gac ttc acc gtg tcc      440
176   Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser
177           115             120             125
179   ggc aac cta ctg ttt atc cga ctg act gct gca gac cac cgc caa ctg      488
180   Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu
181           130             135             140             145
183   cag ctc tcc atc agc tcc tgt ctc cag cag ctt tcc ctg ttg atg tgg      536
184   Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp
185           150             155             160
187   atc acg cag tgc ttt ctg ccc gtg ttt ttg gct cag gct ccc tca ggg      584
188   Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser Gly
189           165             170             175
191   cag agg cgc taa gccagcctg gcgcccttc ctaggtcatg cctcctcccc      636
192   Gln Arg Arg
193           180
195   tagggaatgg tccagcaag agtggccagt tcattgtggg ggcctgattg tttgtcgtg      696
197   gaggaggacg gcttacatgt ttgtttctgt agaaaataaa gctgagctac gaaaaaaaaa      756
199   aaaaaaaaaa a      767
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 180
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 4
210   Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
211           1              5              10              15
213   Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
214           20              25              30
216   Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala

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217          35          40          45
219 Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
220          50          55          60
222 His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
223          65          70          75          80
225 Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe
226          85          90          95
228 Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
229          100          105          110
231 Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
232          115          120          125
234 Ser Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln
235          130          135          140
237 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
238          145          150          155          160
241 Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser
242          165          170          175
244 Gly Gln Arg Arg
245          180

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249 <210> SEQ ID NO: 5
250 <211> LENGTH: 993
251 <212> TYPE: DNA
252 <213> ORGANISM: Homo sapiens
254 <220> FEATURE:
255 <221> NAME/KEY: 5'UTR
256 <222> LOCATION: (1)..(55)
258 <220> FEATURE:
259 <221> NAME/KEY: CDS
260 <222> LOCATION: (56)..(688)
262 <220> FEATURE:
263 <221> NAME/KEY: 3'UTR
264 <222> LOCATION: (689)..(993)
266 <400> SEQUENCE: 5

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C--> 268 gcatactctgt gggccctgac cttctctctg agagccgggc agaggctccg gagcc atg 58
269 Met
270 1
272 cag gcc gaa ggc cag ggc aca ggg ggt tcg acg ggc gat gct gat ggc 106
273 Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly
274          5          10          15
276 cca gga ggc cct ggc att cct gat ggc cca ggg ggc aat gct ggc ggc 154
277 Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly
278          20          25          30
280 cca gga gag gcg ggt gcc acg ggc ggc aga ggt ccc cgg ggc gca ggg 202
281 Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly
282          35          40          45
284 gca gca agg gcc tcg ggg ccg aga gga ggc gcc ccg cgg ggt ccg cat 250
285 Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His
286          50          55          60          65
288 ggc ggt gcc gct tct gcg cag gat gga agg tgc ccc tgc ggg gcc agg 298

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289   Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg
290           70           75           80
292   agg ccg gac agc cgc ctg ctt cag ttg cac atc acg atg cct ttc tcg      346
293   Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser
294           85           90           95
296   tcg ccc atg gaa gcg gag ctg gtc cgc agg atc ctg tcc cgg gat gcc      394
297   Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala
298           100          105          110
300   gca cct ctc ccc cga cca ggg gcg gtt ctg aag gac ttc acc gtg tcc      442
301   Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser
302           115          120          125
304   ggc aac cta ctg ttt atg tca gtt cgg gac cag gac agg gaa ggc gct      490
305   Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly Ala
306           130          135          140          145
308   ggg cgg atg agg gtg gtg ggt tgg ggg ctg gga tcc gcc tcc ccg gag      538
309   Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro Glu
310           150          155          160
312   ggg cag aaa gct aga gat ctc aga aca ccc aaa cac aag gtc tca gaa      586
313   Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser Glu
314           165          170          175
316   cag aga cct ggt aca cca ggc ccg ccg cca ccc gag gga gcc cag gga      634
317   Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln Gly
318           180          185          190
320   gat ggg tgc aga ggt gtc gcc ttt aat gtg atg ttc tct gcc cct cac      682
321   Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro His
322           195          200          205
324   att tag ccgactgact gctgcagacc accgccaaact gcagctctcc atcagctcct      738
325   Ile
326   210
328   gtctccagca gctttccctg ttgatgtgga tcacgcagtg ctttctgccc gtgtttttgg      798
330   ctccaggtcc ctccagggcag aggcgctaag cccagcctgg cgcccccttc taggtcatgc      858
332   ctctctccct aggggaatggt cccagcacga gtggccagtt cattgtgggg gctgattgt
334   ttgtcgctgg agggaggacgg cttacatggt tgtttctgta gaaaataaag ctgagctacg      918
336   aaaaaaaaaa aaaaaa      978
338   <210> SEQ ID NO: 6      993
339   <211> LENGTH: 210
340   <212> TYPE: PRT
341   <213> ORGANISM: Homo sapiens
343   <400> SEQUENCE: 6
345   Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
346       1           5           10          15
348   Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
349           20           25           30
350   Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
351           35           40           45
353   Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
354           50           55           60
356   His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
357           65           70           75           80

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